What is claimed is:

1.

A method of screening animals to determine those more likely to produce larger litters comprising:

obtaining a sample of genetic material from said animal; and

assaying for the presence of a genotype in said animal which is associated with increased litter size, said genotype characterized by the following:

a) a polymorphism in the prolactin receptor gene in said sample which is associated with increased litter size.

2.

The method of claim 1 wherein said step of assaying is selected from the group consisting of: restriction fragment length polymorphism (RFLP) analysis, heteroduplex analysis, single strand conformational polymorphism (SSCP), denaturing gradient gel electrophoresis (DGGE) and temperature gradient gel electrophoresis (TGGE).

3.

The method of claim 1 wherein said step of assaying for the presence of said polymorphism comprises the steps of:

digesting said genetic material with a restriction enzyme that cleaves the prolactin receptor gene in at least one place;

separating the fragments obtained from said digestion;

detecting a restriction pattern generated by said fragments; and

comparing said pattern with a second restriction pattern for the pig prolactin receptor gene obtained by using said restriction enzyme, wherein said second restriction pattern is associated with increased litter size.

4.

The method of claim 3 wherein said restriction enzyme is AluI.

5.

The method of claim 3 wherein said restriction enzyme is HinFI.

6.

The method of claim 3 wherein said restriction enzyme is HypCH4IV.

7.

The method of claim 3 wherein said restriction enzyme is MseI.

8.

The method of claim 1 wherein said animal is a pig.

9.

The method of claim 3 wherein said separation is by gel electrophoresis.

10.

The method of claim 3 wherein said step of comparing said restriction patterns comprises identifying specific fragments by size and comparing the sizes of said fragments.

11.

The method of claim 3 further comprising the step of amplifying the amount of prolactin receptor gene or a portion thereof which contains said polymorphism, prior to said digestion step.

12.

The method of claim 3 wherein said polymorphism is a polymorphic AluI restriction site.

13.

The method of claim 3 wherein said polymorphism is a polymorphic HinFI restriction site.

14.

The method of claim 3 wherein said polymorphism is a polymorphic MseI restriction site.

15.

The method of claim 3 wherein said polymorphism is a polymorphic HypCH4IV restriction site.

16.

The method of claim 12 wherein said restriction site is located in the 3′ coding region of the pig prolactin receptor gene.

17.

The method of claim 13 wherein said restriction site is located in the region between exons 8 and 9 of the prolactin receptor gene.

18.

The method of claim 14 wherein said restriction site is located in the region between exons 8 and 9 of the prolactin receptor gene.

19.

The method of claim 15 wherein said restriction site is located in the region between exons 8 and 9 of the prolactin receptor gene.

20.

The method of claim 11 wherein said amplification includes the steps of:

selecting a forward and a reverse sequence primer capable of amplifying a region pig prolactin receptor gene which contains a polymorphic AluI, HinFI, HypCH4IV, or MseI site.

21.

The method of claim 20 wherein said forward and reverse primers are selected from and based upon SEQ ID NO:3.

22.

The method of claim 20 wherein said primers are SEQ ID NO:4 and SEQ ID NO:5.

23.

The method of claim 20 wherein said primers are SEQ ID NO:6 and SEQ ID NO:7.

24.

The method of claim 22 wherein said forward primer is selected from the group consisting of SEQ ID NO:1 and SEQ ID NO:6 and said reverse primer is selected from the group consisting of SEQ ID NO:2 and SEQ ID NO:6.

25.

The method of claim 22 wherein said primer set comprise SEQ ID NO:1 and SEQ ID NO:2.

26.

The method of claim 20 wherein said primers are from the group consisting of SEQ ID NO:8 and 9; SEQ ID NO:10 and 11, and SEQ ID NO:12 and 13.

27.

A method for identifying a genetic marker for litter size in animals comprising the steps of:

breeding male and female animals of the same breed or breed cross or derived from similar genetic lineages;

determining the number of offspring produced by each female animal;

determining the polymorphism in the prolactin receptor gene of each female animal; and

associating the number of offspring produced by each female animal with said polymorphism thereby identifying a polymorphism for pig litter size.

28.

The method of claim 27 further comprising the step of selecting animals for breeding which are predicted to have increased litter size by said marker.

29.

The method of claim 27 wherein said analysis comprises digestion of PCR amplified DNA with the restriction enzyme selected from the group consisting of AluI, HinFI, HypCH4IV, and MseI.

30.

A primer for assaying for the presence of a polymorphic AluI site in the pig prolactin receptor gene wherein said primer comprises a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, and SEQ ID NO:13.

31.

An allele which is indicative of increased litter size in animals, said allele characterized by the following:

a) is characterized by a polymorphism in the prolactin receptor;

b) is associated with an increase in litter size when present in a female of said animal.

32.

The allele of claim 31 wherein said polymorphism is a restriction site selected from the group consisting of an AluI site, an HinFI site, an MseI site and an HpyCH4IV site.

33.

The allele of claim 32 wherein said polymorphism is located in the 3' translated and nontranslated region of the prolactin receptor gene.

34.

The allele of claim 33 wherein said polymorphism is located in the region between exons 8 and 9 region of the prolactin receptor gene.

35.

A DNA sequence from the pig prolactin receptor gene 3' translated and nontranslated region, said sequence consisting of SEQ ID NO:3.

36.

A method for screening pigs to determine those more likely to produce larger litters, and/or those less likely to produce larger litters, which method comprises of the steps:

determining the alleles of prolactin receptor present in a pig;

determining the alleles of other markers for genes known to affect litter size; and

selecting for animals with favorable combinations of alleles and against those carrying unfavorable combinations.

37.

The method of claim 36 wherein the determination of prolactin receptor alleles comprises determining the presence of at least one allele associated with at least one DNA marker linked either directly or indirectly to prolactin receptor.

38.

The method as claimed in claim 36 wherein the DNA marker is a microsatellite.

39.

The method as claimed in claim 36 wherein the DNA marker is SW1305, S0077, S0006, SW2411, SW1035 and S0111.

40.

A method of screening animals to determine those more likely to produce larger litters comprising:

obtaining a biological sample from said animal; and

assaying for the presence of a genotype in said animal which is associated with increased litter size, said genotype characterized by a polymorphism in the prolactin receptor gene wherein said polymorphism identifiable by a PCR protocol selected from the following:

amplification with four contiguous bases from each of SEQ ID NO:8 and SEQ ID NO:9 and HinFI digestion,

amplification with four contiguous bases from each of SEQ ID NO:12 and SEQ ID NO:13 and MseI digestion;

amplification with four contiguous bases from each of SEQ ID NO:1 and SEQ ID NO:2 and AluI digestion;

amplification with four contiguous bases from SEQ ID NO:10 and SEQ ID NO:11 and HpyCH4IV digestion.